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M. auratus mRNA for al G.gallus Prx-2 (S8) m gMHox=homeobox (chick Gallus gallus paired-

Rat cartilage homeopr Mus musculus homeobox

Carassius auratus hom

Xenopus laevis homeob M.musculus Otxl mRNA. Xenopus laevis orthod

MUSCHX10A MMODEXZ MUSCHX12 MMODEXZ HS031986 RATCARTIX MMO03873 CAMO7056 MAALX3 GGPRX2 SG9088 CCHKPRX1 XLXOTX21 XLXOTX21 XLXOTX11 XLXOTX11 XLOTX10C SG9508 XELORTHOAA XLOTXNUC SG9508 SEFOTX2 SEFOTX2 SEFOTX3 S

X.laevis mRNA for hom Pax-6-transcription f Zebrafish otx2 mRNA f Zebrafish otx2 mRNA f

Rattus norvegicus pai Human homeobox protei Mus musculus (clone 6 M.musculus Otx2 mRNA. M.musculus mRNA for h Mus musculus MHox pro

RNU29174 HUMPHOX1A

X.laevis organizer sp 1.
Rattus norvegicus OTS 5.
Danio rerio orthodent 5
Schistosoma mansoni p 3.
Kenopus laevis cartil 3.
Sea urchin late gastr 4
Drosophila melenogast

Drosophila melanogast Drosophila melarogast D.melanogaster mRNA f C. coturnix mRNA for B.rerio mRNA for Pax[B.rerio pax-6 mRNA. Paracentrotus ilvidus.

DMU52968 DMU52968 DM52968

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H.sapiens oculorhombi Human paired box gene Mouse Pax-3 gene for

MMPHOXH HUMOCLHMB HUMPAX6AN MMPAX3R RNU69644 RNU69644

Rattus norvegicus Pax Rattus norvegicus Pax

Xenopus laevis goosec Pax-6 [rats, small ey

PLU14621 XELGSCHB S74393 BRPAXZFA BRPAX6

M.musculus Phox2 mRNA

rk2=glial-specific ho D.melanogaster mRNA f

S78747 DMREPO

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l (bases ito 2399)
Saito, T., Greenwood, A., Sun, O. and Anderson D. J.
TUBELTRICATION by differential RT-PCR of a novel paired homeodomain protein specifically expressed in sensory neurons and a subset of their CNS targets
Mol. Cell. Neurosci. 6 (3), 280-292 (1995) ıs ochondrial eukaryotes; Metazoa; Chordata; heria; Rodentia; Sciurognathi; Myomorpha; Muridae; Amy Greenwood, Biology, Caltech, 216-76 19 bp mRNA ROD 10-FEB-1996 is paired-like homeodomain transcription factor mplete cds. (bases 1 to 2399) to_I - Greenwood, A.L., Sun, Q. and Anderson, D.J. ALIGNMENTS Submitted (14-JUN-1995) TITLE JOURNAL REFERENCE AUTHORS TITLE MEDLINE REFERENCE AUTHORS JOURNAL

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Mean 12.749; Variance 9.680; scale 1.317

Statistics:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PSSHPRAALDGLAPGHLLAARSVLSPAQYGSMGLLGPGGLPGFYTQPTFLEVLSDPQS
VHLQPLGRASGPLDTSQTASSDSEDVSSSDRKMSKSALNQTKKRKKRRHRTIFTSYQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        p mRNA ROD 12-JAN-1995
6) homeobox protein (Chx10) mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mirinae: Mus.
1 (bases 1 to 3089)
1 (bases 1 to 3089)
1 u. L.S., Chen, J.D., Ploder, L., Vidgen, D., van der Kooy, D.,
Rainins, Y. I. and McInnes, R.R.
Developmental expression of a novel murine homeobox gene (Chx10):
evidence for roles in determination of the neuroretina and inner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     376 AGCGCAGAAATCGGACAACCTTCGCTCTTCAGCAGTTGGAAGCTCTGGAGGCAGTCTTTG 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     503 atgaagcccactacccagatgtctacgcccgggagatgctggccatgaaaacggagctcc 562
                                                                                                                                                                                                                                                                                                                                                             443 agoggogacacaggacaatotttacttoctaccagotagaggagotggagaaagcattca 502
                                                                                                                     280 gictitgagoggacacactaiccigaigcittigigogagaagacciigccogcogggig 339
                                                                                                                                                                                                                                                                              369 AGAAAACAGCGCAGAAATCGGACAACCTTCGCTCTTCAGCAGTTGGAAGCTCTGGAGGCA 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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Pred. No. 1.02e-21;
Length 1433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches 50; Indels
                                                         0; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (strain CD1/129sv) cDNA to mRNA. Mus musculus
Score 82; DB 78; Pred. No. 1.07e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EKPEEEDATEEDRPAEKLSPPQLEDMA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/strain="CD1/129sv"
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NID KEYWORDS SOURCE ORGANISM

AUTHORS TITLE JOURNAL

REFERENCE

REFERENCE

AUTHORS

TITLE

JOURNAL MEDLINE REMARK

COMMENT

DEFINITION

RESULT

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ACCESSION

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/organism="Mus musculus"
/clone_lib="lambda-gt10 of 8.5 day embryos"
/clone_start=1
/codon_start=1
/product="Dna-binding protein"
/product="PiD:951362"
/db_xref="FiD:951362"
/db_xref="SMISS-PROT:P4371"
/translation="MISSYGHVLERQPALGGRLDSPGNLDTLQAKKNFSVSHLLDLEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGDMVAAQADESVGEAGRSLLESPGLTSGSDTPQQDNDQLNSEEKKKRKQRRNRTTFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSOLQALERVFERTHYPDAFVREDLARRVNLTEÄRVQVWFQNRRAKFRRNERAMLANK
NASLLKSYSGDVTAVEQPIVPRPAPRPTDYLSWGTASPYSAMATYSATCANNSPAGGI
                                                                                       Direct Submission
Submitted (07-APR-1992) M. Kern, Childrens Hospital Res Foundation,
Basic Science Research, Elland and Bethesda Aves, Cincinnati, Ohio
45229-2899, USA
                                                                                                                                                 2 (bases 1 to 949)
Kern,M.J., Witte,D.P., Valerius,W.T., Aronow,B.J. and Potter,S.S.
A novel murine homeobox gene isolated by a tissue specific PCR
cloning strategy
Nucleic Acids Res. 20 (19), 5189-5195 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MHOX:a mesodermally restricted homeodomain protein that binds an essential site in the muscle creatine kinase enhancer Development 115, 1087-1101 (1992)
      Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          369 AGAAAACAGGGCAGAAATCGGACAACCTTCGCTCTTCAGCAGTTGGAAGCTCTGGAGGGCA 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 429 GICITIGCCCAAACACACTACCCAGAIGTCTTCACCAGAGAAGAGCTAGCCAIGAAAATA 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       415 agaaagcagcggagaaacaggacaacattcaacagcagccaactgcaggccttggagcgt 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Murinae; Mus.
1 (bases 1 to 1066)
Cserjesi,P., Lillly,B., Bryson,L.J., Wang,Y., Sassoon,D.A. and
OISON,E.N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gtetttgageggaeacattacceggatgettttgttcgagaagatetegeacgtegggtg
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Mus musculus (library: C2 gtll) cDNA to mRNA.
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 949;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 72; DB 81; Length 949
Pred. No. 7.40e-18;
0; Mismatches 59; Indels
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420..600
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279 c 254 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 3.0%;
Best Local Similarity 68.9%;
Matches 131; Conservative
                                                 (bases 1 to 949)
                                                                                                                                                                                                                                                                                                                                 . 949
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                                                                                                                                                                                                                                                                                                                                 source
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ORIGIN
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                                            REFERENCE
AUTHORS
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AUTHORS
TITLE
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MEDLINE
FEATURES
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AUTHORS
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FEATURES
                                                                                                             JOURNAL /
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INLPESRVQVWFKNRRAKCRQQQQ"
inlpesrvqvwFknrrakCRQQQQ"
inlpesrvqvwFknrrakCrqqqqq"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     B, Via Guglielmo Marconi
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                                                                                                                                                                                                                                                                                                                        Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptide sequences only
See X68883-4 for mouse Otx genes related to Orthodenticle, a
Drosophila gene important for controlling head development. (See
also X68879-X68882).
                                     Nested expression domains of four homeobox genes in developing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  436 CCCAAACACACTACCCAGATGTCTTCACCAGAGAAGAGCTAGCCATGAAAATAAACCTCA 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79 tttgccaagacccggtacccagacatcttcatgagggaagaggtggcactgaaaatcaac 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19 aaacagcgaagggagaggacgacttttactagggcacagctcgacgttctggaagctctg 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-DEC-1993
                                                                                                                                                                         02-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (12-JAN-1993) A. Simeone, I G B, Via Guglieli
10, 801 25 Napoli, ITALY
2 (bases 1 to 204)
Simeone, A., Acampora, D., Gulisano, M., Stornaluolo, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    house mouse.
Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
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Pred. No. 8.15e-19;
0; Mismatches 48; Indels
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                                                                                                                                                                         ROD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/dev_stage="11-day old embryo"
<1..>204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MAHOBOXG 949 bp RNA
M.musculus mRNA for homeobox gene.
X59725 M91544 S47170
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                                                                                                                                                                   M.musculus Otx2 mRNA.
X68884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 3.1%;
Best Local Similarity 71.8%;
Matches 122; Conservative
                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 204)
                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                          homeobox gene.
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                                                                                                                                                                                                                                                                                                                                                                       Murinae; Mus.
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                                                                                                                                                                                                                                                                                                    Mus musculus
                                                                                                                                                                                                                                                                                house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                           Simeone, A.
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DEFINITION
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BASE COUNT ORIGIN

CDS

FEATURES

KEYWORDS SOURCE ORGANISM

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/product="cart-1"
/db_xref="pid:q1098654"
/db_xref="pi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       426 GCAGTCTTTGCCCAAACACACTACCCAGATGTCTTCACCAGAGAAGAGCTAGCCATGAAA 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     540 agcagtaagaaacggaggcaccgaaccacttcaccagtttgcagctagaggagctggag
/note="cartilage-specific homeodomain protein"
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Zhao, G.-Q., Zhou, X., Eberspaecher, H., Solursh, M. and
Crombrugghe, B.
                                                                                                                                                                                                                                                                                                                                                                                                      Length 1442;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           U.S.A. 90, 8633-8637 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                Score 72; DB 74;
Pred. No. 7.40e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cell_type="chondrocyte"
/tissue_type="chondrosarcoma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                            'note="encodes homeodomain"
                                                                                                                                                                                                                                                                                                                        358 t
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/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chondrocytes
Proc. Natl. Acad. Sci. 93391409
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larity 69.8%;
Conservative
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es 127; Conserv
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Gordon, D.F., Wagner, J., Atkinson, B., Chlono, M., Berry, R., Sikela, J.
and Gutierrez-Hartmann, A.
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Human cartilage-specific homeodomain protein Cart-1 mRNA, complete
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Gordon, D.F., Wagner, J., Atkinson, B.L., Chiono, M., Berry, R.,
Sikela, J. and Gutlerrez-Hartmann, A.
Human Cart-1: structural organization, chromosomal localization,
and functional analysis of a cartilage-specific homeodomain cDNA
DNA Cell Biol. 15 (7), 531-541 (1996)
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Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 7.40e-18;
0; Mismatches 59; Indels
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                                                     /ceil_line="C2C12"
/ceil_type="myeloblast"
/tissue_lib="C2 gt11"
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181..834
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Best Local Similarity 68.9%;
Matches 131; Conservative
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/db_xref-*PiD:9413751*
/db_xref-*PiD:9413751*
/translation=*MEFLSEKFALKSPPSKNSDFYMGTGGALEHVMETLDNESFYGKA
TAGKCVQAFCPPLPRAEHHVRLDRTSPCQDSSYNNGTIKVEGQPLHTELNRAMOGCNNL
RMSPVKGMPEKSELDELGDKCDSNVSSSKRRRHRTTFTSLQLEELEKVPGKTHYPDVY
PKGDALAFTELTEARVQVWFQNRRAWRRKRENGTGQIQQAKSHRAATVIDISJVLPRTDSY
PQIQNNLWAGNTSGGSVYTSCHLPRDASSCHMPYSHSPRTDSSYTGFSNHQNGFGHVP
LNNFFTDSLLTGTTNGHAFETKPEFERRSSSIAVLRWKAKEHTANISWAM*
                                                                                                                                                           DNA-binding protein; homeoprotein 1; transcription factor. Rattus norvegicus chondrosarcoma cDNA to mRNA. Rattus norvegicus sattus norvegicus Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
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02-NOV-1993
                 Rat cartilage homeoprotein 1 (Cart-1) mRNA, complete cds L14018
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Query Match 3.0%;
Best Local Similarity 68.9%;
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NASLLKGYSGDVTAWCDPIVPRRARPTPTLSWGTASPYRSSSLPRCCLHEGLHNGF"
order[1262,1438,1620,1692)
/note="introns appear at these places in the genomic
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Kern,M.J., Argao,E.A., Birkenmeier,E.H., Rowe,L.B. and Potter,S.S.
Genomic organization and chromosome localization of the murine
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
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Location/Qualiflers
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                                                                              905 aaggtettecaaaaaaggattaeceggatgtatatgteagagaacagettgeactgaga 964
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   Length 1760;
Score 72; DB 86; Length 176
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/gene="Pmx"
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Best Local Similarity 69.1%;
Matches 130; Conservative
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Kern, M.J.
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Vertebrata; Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Ostariophysi; Cypriniformes; Cyprinoidea; Cyprinidae;
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Submitted (23-FEB-1994) Edward M. Levine, Health Sciences Center,
SUNY at Stony Brook, Stony Brook, NY 11794, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                     1295 agaaagcagcggagaaacaggacaacattcaacagcagccaactgcaggccttggagcgt 1354
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                                                                                                                                                                                                        429 GTCTTTGCCCAAACACACTACCCAGATGTCTTCACCAGAGAAGAGCTAGCCATGAAATA 488
                                                                                                                                 369 AGAAAACAGCGCAGAAATCGGACAACCTTCGCTCTTCAGCAGTTGGAAGCTCTGGAGGCA 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        369 AGAAAACAGCGCAGAAATCGGACAACCTTCGCTCTTCAGCAGTTGGAAGCTCTGGAGGCA 428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                465 aggaaaaagcgaaggcacaggacagtctttacctcacatcaacttgaggaactggagaaa 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAU07056 1588 bp mRNA VRT 22-OCT-1994
Carassius auratus homeobox protein mRNA, complete cds.
U07056
9460927
                                               Gaps
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Pred. No. 2.22e-17;
0; Mismatches 58; Indels
Length 3359;
Score 72; DB 82; Length 335
Pred. No. 7.40e-18;
0; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 1588)
Levine, E.M., Hitchcock, P.F., Glasgow, E. and :
Restricted expression of a new paired-class !
and regenerating adult goldfish retina
J. Comp. Neurol. 348 (4), 596-606 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     auratus,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="retina"
/dev_stage="adult"
30..1055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Carassius
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     373 g
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Best Local Similarity 69.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 1588)
                                            131; Conservative
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29-MAR-1996

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RESULT

DEFINITION

ACCESSION

KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

REFERENCE AUTHORS

TITLE

JOURNAL MEDLINE FEATURES

CDS

BASE COUNT

OREGIN

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RPTALSPEYLSWSSSSPYSTVPSYSSSGTATAAQGVNMANSIASLRLKAKEFELHQNO
                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (10-JUN-1994) F. Meijlink, Netherlands Inst. for
Developmental, Biology, Hubrecht Laboratory, Uppsalalaan 8, 3584 CT
Utrecht, NETHERLANDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Gallus gallus"
Adv_stage="10 days"
/clone_lib="lambda gill chicken embryō libraries one from clontech and one from Karolinska Institute"
                                                                                                                                                                                                                                 Leussink, B., Brouwer, A., el Khattabi, M., Poelmann, R.E., dittenberger-de Groot, A.C. and Meijlink, F. Expression patterns of the paired-related homeobox genes MHox/Prxl and S8/Prx2 suggest roles in development of the heart and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Olson, E.N. The expression pattern of the chick homeobox gene gMHox suggests role in patterning of the limbs and face and in compartmentalization of somites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gallus sp.
Unclassified.
1 (bases 1 to 895)
Kuratani,S., Martin,J.F., Wawersik,S., Lilly,B., Eichele,G. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43 aaacagaggaggaaccgcaccacattcaacagcagccaactgcaggctctggagagggtc 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           372 AAACAGGGGAAAATCGGACAACCTTCGCTCTTCAGCAGTTGGAAGCTCTGGAGGCAGTC 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103 tttgagoggacacattaccccgacgccttcgtgcgggaggagctggccaggaggtgaac 162
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gMHOx=homeobox [chickens, stage 17 embryo, heart, mRNA, 895 nt
869088
g545359
                                                                                                                                               Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Archosauria; Aves; Neognathae; Galliformes;
Phasianidae; Phasianinae; Gallus
1 (bases 1 to 849)
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0; Mismatches 50; Indels
    VRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      153 t
                                                                                                                                                                                                                                                                                                                                   Mech. Dev. 52 (1), 51-64 (1995)
96076127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
      RNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      222
               G.gallus Prx-2 (S8) mRNA.
X79695
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      849 bp
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Best Local Similarity 70.4%;
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Meijlink, F.
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                                                                                                                             Gallus gallus
                                                                                      Prx-2 dene.
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                                                                   9558376
                                                                                                          chicken
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                                                                                                        SOURCE
ORGANISM
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ACCESSION
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MEDLINE
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPRGPRLSREPACGPLEPYLPEPAKPPAKYLQDLGPAPVLNGGHFYEGPAEAEEKASK
AASFPQLPVDCRGGPRDGPSNVQGSPGPCLASLRVPLSPGLPDTWELAKSKSKKRRNR
TTFSTFQLEELEKVFQKTHYPDVYAREQLALRTDLTEARVQVWFQNRRAKWRERYG
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YSHSHGNVAGFWGVPASPAAHPGIYSIHGFPPALGGHSFEPSPDGDYKSPSLVSLRVK
                                                                                                                                                                                                                                                                                                           9387455
alx3 gene.
glolden hamster.
Mesocricetus auratus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
Cloctinae; Mesocricetus.
1. (bases 1 to 1744)
German, M.S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (05-SEP-1994) M.S. German, HORMONE RESESEARCH INST.,
UNIVERSTIY OF CALIFORNIA SAN FRANCISCO, HSW 1090, BOX 0534, SAN
FRANCISCO, CA 94143-0534, USA
2 (bases 1 to 1744)
                                       540 gtettecagaaaacecaetaeceggaegtgtatgeeegaagageagetggetttaeggeaeg 599
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      369 AGAMAACAGCGCAGAMATCGGACAACCTTCGCTCTTCAGCAGTTGGAAGCTCTGGAGGCA 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rudnick, A., Ling, T.T., Odagiri, H., Rutter, W.J. and German, M.S. Pancreatic beta cells express a diverse set of homeobox genes Proc. Natl. Acad. Sci. U.S.A. 91 (25), 12203-12207 (1994)
                                                                                                                                                                                                                                                     30-MAR-1995
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Pred. No. 6.65e-17;
0; Mismatches 55; Indels
                                                                                                                                                                                                                                                       800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="pancreatic islet"
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21..1061
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1..1744
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Best Local Similarity 69.4%;
Matches 125; Conservative
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09-FEB-1995

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Anterior neurectoderm is progressively induced during gastrulation: the role of the Kenopus homeobox gene orthodenticle Development (1995) in press 2 (bases 1 to 1264)
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FTRAQLDILEALFAKTRYPDIFMREEVALKINLPESRVQVWFKNRRAKCRQQQQQON
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SDPLSTSSSCWQRSYPWTYTQASGYSQGYASSTSYFGGMDCGSYLTPWHHQLSGPGAT
LSPWSTNAVTSHLNQSQAALSSQAYGASSLGFNSTADCLDYKDQTASWKLNFNADCLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
Pipidae; Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (12-JAN-1995) Ira Blitz, Developmental and Cell Biolo
and the Developmental Biology Center, University of California,
Irvine, CA 92717-2300, USA
                                                                                                                                                                                                                                                                                                                                368 AAGAAAACAGCGCAGAAATCGGACAACCTTCGCTCTTCAGCAGTTGGAAGCTCTGGAGGC 427
                                                                                                                                                                                                                                                                                                                                                                                                            565 ggtctttgagaggacacactacccgatgcctttgtacgggaagaccttgcacgcagagt 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <1..122
213..1082
//gene="xotx2"
//note="xotx2"
/note="missexpression of xotx2 induces ectopic cement
glands; homeodomain protein"</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xenopus laevis homeobox protein orthodenticle 2 (Xotx2) mRNA, Complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                  428 AGTCTTTGCCCAAACACACTACCCAGATGTCTTCACCAGAGAAGAGCTAGCCATGAAAAT
    /product="paired-related homeotic gene product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1084;
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Pred. No. 1.98e-16;
0; Mismatches 52; Indels
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                                                                                                                                                    /gene="Prx-1"
/note="homeobox"
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Blitz,I.L. and Cho,K.W.Y.
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Best Local Similarity 69.9%;
Matches 121; Conservative
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African clawed frog.
Xenopus laevis
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/translation-"RASSYAHAMEROALLPARLDGFAGLDNLQAKKNESVSHLLDLEE
AGDWVAAQGBEGGEBEGRELESPGITSGSDTPOQDNDQLNSEEKKKRRQRRNRTTFN
SSQLQALERVEETHYPDAFYREDLERYNLTEARVOWFQNRAKFRNBRAMIASK
NASLLKSYSGOVTAROPIVPRPAPRFIDYLSWGTASFYSANATYSTTCTNASPAQGM
NAANSIANAKAKEYSLQRNQVPTVN"
                                                                                                                                /organism="Gallus sp."
31..768
/gene="gMHox"
/note="Description: homeobox; homeodomain protein; Method:
                                                                                                                                                                                                             conceptual translation supplied by author. This sequence comes from Fig. 1A"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ., Koyama, E., Myokai, F., Taniguchi, S., Ohuchi, H., Saito, T.
                                  Genbank staff at the National Library of Medicine created this entry [NCBI glabbg 144347] from the original journal article. This sequence comes from Fig. 1A. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 363 ggtctttgagagacacactaccccgatgcctttgtacgggaagaccttgcacgcagagt 422
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Gallus gallus (library: lambda gt10) stage 24-26 cDNA to mRNA,
clones p2 and p7.
Gallus gallus
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1 (bases 1 to 1084)
Noho,T., Koyama,E., Myokai,F., Taniquchi,S., Ohuchi, H...
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Dev. Biol. 158, 254-264 (1993)
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. Biol. 161 (2), 357-369 (1994)
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0; Gaps Query Match 2.8%; Score 67; DB 51; Length 1264; Best Local Similarity 69.4%; Pred. No. 1.75e-15; Matches 120; Conservative 0; Mismatches 53; Indels (

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159:EST159
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                                                                                                                                                                                                                                                                                                                                                                              Release 2.1D John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
Distribution rights by IntelliGenetics, Inc.
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.cs: Mean 12.474; Variance 4.448; scale 2.805

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result.being printed, and is derived by analysis of the total score distribution.

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Human fetal brain cDN 2.63e-09

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236 gcacatctagctgcgcccgagtgaacgtcgtcctccccggngctgttt 284
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                                                                                                                       AA022576 498 bp mRNA EST 09-AUG-1996 2e72610.rl Soares fetal heart NbHH19W Homo sapiens cDNA clone 364554 5' similar to SW:MHOX_MOUSE Q02810 HOMEOBOX PROTEIN MHOX. ; .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into (The Not I and Eco RI sites of a modified pT773 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung
    Human fetal brain cDN 2.63e-09
zn71g01.s1 Stratagene 1.73e-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 478.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              338 cggtgaggttcaccccggcgggcaaggtcttctcgcacaaagcatcaggatagtgtgtc 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      558 CTCTCTCTCTTCTTCCTCCACTTGGCTCTTCGGTTCTGGAACCAAACCTGCACTCTGGCTT 499
                                                                                                                                                                                                                                                                                         Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 498) Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Rucaba,T., Le,M., Lenon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Wilson RK
Washu-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 76; DB 26; Length 498;
Pred. No. 2.79e-46;
0; Mismatches 54; Indels
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/lab_host="DH10B (ampicillin resistant)"
<1...>498
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                                                                               ALIGNMENTS
430 43 C14394
491 233 HSAA1273
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Best Local Similarity 71.2%;
Matches 136; Conservative
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W22594 829 bp mRNA EST 06-MAY-1996
70B5 Human retina cDNA Tsp5091-cleaved sublibrary Homo sapiens cDNA
not directional.
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176 gtgccacctcctcgcatgaagatgtctgggtaccgggtcttggcaaacagtgcttcca 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryotze; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutherla; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 829)
Macke, J., Smallwood, P. and Nathans, J.
Adult Human Retina cDNA.
Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dept. of Molecular Biology and Genetics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Dr. Jeremy Nathans
Dr. Jeremy Nathans, Dept. of Molecular Biold
Johns Hopkins School of Medicine
725 North Wolfe Street, Baltimore, MD 21205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 410 955 4678
Fax: 410 614 0827
Email: jeremy_nathans@qmail.bs.jhu.edu
Clones from this library are NOT available.
PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FORWARD: CTTTTGAGCAAGTTCAGCCTGGTTAAGT
BACKWARD: GAGGTGGCTTATGAGTATTTCTTCCAGGGTAA
Seq primer: GGGTAAAAAGCAAAAGAATT.
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Pred. No. 3.45e-41;
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Matches 119; Conservative
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                                                                                                  458 cgctgctttct 468
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Section of the Section of

Homo sapiens

SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

g1299427 human.

DEFINITION

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ACCESSION KEYWORDS PRimers

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FEATURES

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Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
                                                             Deuterostomia; Chordata; Vertebrata; Gnathostomata; Ostelchthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 324)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Hulman,M., Rucaba,T., E.M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Treyaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                367 GAAGAAAACAGCGCAGAAATCGGACAACCTTCGCTCTTCAGCAGTTGGAAGCTCTGGAGG 426
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WashU-Merck EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                           Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"/clone="230882"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: estewatson.wustl.edu
High quality sequence stops: 180
Source: IMAGE Consortium, LLNL
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Matches 118; Conservative
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                                                                                   W22594 829 bp mRNA EST 06-MAY-1996
70B5 Human retina cDNA Tsp509I-cleaved sublibrary Homo sapiens cDNA
not directional.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Human retina cDNA Tsp5091-cleaved sublibrary"
/sex="mixed (males and females)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  yt83cO2.rl Homo sapiens cDNA clone 230882 5' similar to gb:M93650 PAIRED BOX PROTEIN PAX-6 (HUMAN);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 acttagctcttcgattcttaaaccatacctgcaccctcgactcgggcangttgattttca 175
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                                                                                                                                                                                                                                                                         Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 829)
Macke, J., Smallwood, P. and Nathans, J.
Adult Human Relina cDNA
Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                            Dr. Jeremy Nathans, Dept. of Molecular Biology and Genetics
Johns Hopkins School of Medicine
725 North Wolfe Street, Baltimore, MD 21205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 71; DB 186; Length 829;
Pred. No. 3.45e-41;
0; Mismatches 50; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 410 955 4678
Fax: 410 614 0827
Email: jeremy_nathans@qmail.bs.jhu.edu
Clones from this library are NOT available.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FORWARD: CTTTTGAGCAAGTTCAGCCTGGTTAAGT
BACKWARD: GAGGTGGCTTATGAGTATTTCTTCCAGGGTAA
Seg primer: GGGTAAAAAGCAAAAGAATT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="retina"
/dev_stage="adult"
/lab_host="E. coli strain K802"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               194 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism-"Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             218 9
                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Dr. Jeremy Nathans
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Query Match 2.9%; Best Local Similarity 70.4%; Matches 119; Conservative

DEFINITION

RESULT

236 420

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184 c

mRNA ..SE COUNT ORIGIN

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was primed with a Not I - oligo(dT) primer (5'
                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
...572
...572
Sequence 572 BP; 122 A; 189 C; 164 G; 97 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: -28M13 rev2 from Amersham High quality sequence stop: 464.
Location/Qualifiers
1.572
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AA033108
g1504502
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ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
JOURNAL
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 386)
Adams, M.D., Soares, M.B., Kerlavage, A.R., Fields, C. and Venter, J.C.
Rapid CDNA sequencing (expressed sequence tags) from a
directionally cloned human infant brain cDNA library
Nature Genet. 4, 373-380 (1993)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       agaaatagaacatcctttacccaagagcaaattgaggccctggagaaagagtttgagaga 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91504502
42 ANG-1996 (Rel. 49, Created)
24-ANG-1996 (Rel. 49, Last updated, Version 1)
m126903.rl Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA
clone 464692 5' similar to gb:X52875 Mouse homeobox gene S8 mRNA
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Dubuque T., Geisel S., Kucaba T., Lacy M., Le M., Martin J.,
Morris M., Schellenberg K., Steptoe M., Tan F., Underwood K.,
Moore B., Theising B., Wylle T., Lennon G., Soares B., Wilson R.,
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Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 386;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 60; DB 131; Length 38
Pred. No. 2.94e-30;
0; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Adams, MD
The Institute for Genomic Research
932 Clopper Road, Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             11
                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/clone="HIBBQ26"
98 c 80 g 77
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                                                                                                                                                                                                                                                                                                                   Email: mdadams@tigr.org.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Waterston R.; "The WashU-HHMI Mouse EST Project";
                                                                                                                                                                                                                                                                                                                                                                                                                                                             80 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 2.5%;
Best Local Similarity 68.3%;
Matches 112; Conservative
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MMA33108
AA033108;
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ORIGIN
                                                     AUTHORS
TITLE
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                            REFERENCE
                                                                                                                                 JOURNAL
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T 3'], on equal amounts ofmRNA from 2 13.5dpc and 2 14.5dp
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M.; Martlin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Inderwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Schelsen, Wilson, R. and
                                                                                                                                                                         adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of themodified pTTT3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."

/clone="kd64692"
/clone=lib-"Soares mouse embryo NbME13.5 14.5"
/sex="unknown"
                                                                       embryos [total RNA provided by Minoru Ko, Wayne State Univ., from 2 ]; double-stranded cDNA was ligated to Eco
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              372 AAACAGCGCAGAAATCGGACAACCTTCGCTCTTCAGCAGTTGGAAGCTCTGGAGGCAGTC 431
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WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 572;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 2.3%; Score 55; DB 240; Length 57:
Best Local Similarity 66.3%; Pred. No. 1.92e-25;
Matches 112; Conservative 0; Mismatches 57; Indels
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T 3'], on equal amounts of mRNA from 2 13.5dpc and 2 14.5dpc embryos [total RNA provided by Minoru Ko, Wayne State Univ., from 2 ]; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacla), digested with Not I and cloned into the Not I and Eco RI sites of the modified normalization, and was constructed by Bento Soares and M.Fatina Bonaldo."
                                                                                                        l (bases 1 to 424)
Marra,M., Hillter,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schallenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W17990 424 bp mRNA EST 10-SEP-1996 mb82e05.rl Soares mouse p3NMF19.5 Mus musculus cDNA clone 335936 5' similar to gb:U03873 Mus musculus homeobox (MOUSE);.
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113 aagcagcgcggaatcgaaccacttcaacagcagccagctgcaggcgctggagcgtgta 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         432 TTTGCCCAAACACACTACCCAGATGTCTTCACCAGAGAAGAGCTAGCCATGAAATAAAC 491
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Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Soares mouse embryo NbMEl3.5 14.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 604;
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                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 55; DB 182; Lo
Pred. No. 1.92e-25;
0; Mismatches 57;
Seg primer: -28M13 rev2 from Amersham
High quality sequence stop: 460.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Marra M/Mouse EST Project
                                                     1..604
/organism="Mus musculus"
/strain="C57BL/6J"
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The WashU-HHMI Mouse EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.3%;
Similarity 66.3%;
.12; Conservative
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112;
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                               Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

The Wash U-HHMI Mouse EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:25543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, NO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                /clone="464692"
/clone_lib="Soares mouse embryo NbME13.5 14.5"
/sex="unknown"
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Pred. No. 1.92e-25;
0; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                  /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH108"
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 /organism-"Mus musculus"
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Best Local Similarity 66.3%;
Matches 112; Conservative
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                                                                                                                                                                                                                    W17990 424 bp* mRNA EST 29-APR-1996 mD82e05.rl Soares mouse p3NWF19.5 Mus musculus cDNA clone 335936 5' similar to gb:U03873 Mus musculus homeobox (MOUSE);.
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwook,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Pred. No. 1.71e-24;
0; Mismatches 28; Indels
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                                               Inno. 2. Control of the control of t
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Best Local Similarity 74.5%;
Matches 82; Conservative
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AA022577 513 bp mRNA EST 09-AUG-1996 ze72e10.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 364554 3' similar to SW:HPRI_CHICK Q05437 HOMEOBOX PROTEIN PRX-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ctttgagcggacacattacccggatgctttgttcgagaagatctcgcacgtcgggtgaa 60
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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Naterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Wilson RK
WashU-Merck EST Project
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
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Pred. No. 1.71e-24;
                                               /organism-"Mus musculus"
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Location/Qualifiers
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The WashU-Merck EST Project
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Best Local Similarity 74.5%;
Matches 82; Conservative
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Sus scrofa
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Artiodactyla; Sulformes; Suina; Suldae; Sus.
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Winteroe, A.K., Fredholm, M. and Davies, W.
Evaluation and characterization of a porcine small intestine CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (26-JUL-1995) Winteroe A.K., The Royal Veterinary and Agricultural University, Department of Animal Science and Animal Health, Division of Animal Genetics, Bulowsvej 13, 1870 Frederiksberg C, DENMARK

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="small intestine"
/clone_lib="directionally cloned cDNA in XL1-blue MRF'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 456 GTCTTCACCAGAGAAGAGCTAGCCATGAAATAAACCTCACAGAAGCAGAGTGCAGGTT 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    230 atgtccactcgcgaagaaatcgccgtgtggaccaaccttacggaagcccgagtccgggtt 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S.scrofa mRNA; expressed sequence tag (5'; clone clell). F14521
                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Soares mouse embryo NbME13.5 14.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 439;
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                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
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MGI:233133
Seq primer: ETPrimer
High quality sequence stop: 347.
Location/Qualifiers
                                                                                             /organism="Mus musculus"
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2 (bases 1 to 372)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  132 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST; expressed sequence tag
                                                                                                             /strain="C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                  /sex="unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                  <1..>439
124 c
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Direct Submission
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        1 (bases 1 to 439)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Thelsing,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W59350 439 bp mRNA EST 06-JUN-1996 md49b07.rl Scares mouse embryo NbMEl3.5 14.5 Mus musculus CDNA clone 371701 5' similar to PIR:S52424 S52424 homeodomain protein unc-30 - Caenorhabditis elegans ;.
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Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 286 tgtctttgagoggacacactatcctgatgctttgtgcgagaagaccttgcccgccgggt 345
                                                                                                                                                                                                                                                                                                                                                                                                                                  428 AGICITIGCCCAAACACACTACCCAGAIGICTICACCAGAGAGAGAGCTAGCCAIGAAAAT 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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2
                                                                                                                                                                                    Length 513;
                                                                                                                                                                                                                                                                                                                                                               Score 53; DB 26; Length 513
Pred. No. 1.51e-23;
0; Mismatches 54; Indels
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Best Local Similarity 69.7%;
Matches 136; Conservative
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/note="expressed sequence tag"
/note="homolog to alx3 gene product; Mesocricetus auratus"
Sequence 372 BP; 94 A; 112 C; 114 G; 43 T; 9 other;
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/tissue_type="small intestine"
/clone_lib="directionally cloned cDNA in XLI-blue MRF'"
/clone=clell*
<1..>372
/partial
                                                                                                                                                                                                                                                                                                                                                                   200 agoggaggatocgaaccacattcaccacagagcagctgcaggagctggagaagatcttcc 259
                                                                                                                                                                                                                                                                                                                                                                                                   260 atttcacccactaccccgatgtccatatccgcaaccagctngnagccaggntcaacctnc 319
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                                                                                                                                                                                                                                                                                                                 0; Gaps
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Pred. No. 7.98e-20;
0; Mismatches 65; Indels 0; Gaps
                                                                                        //octe="expressed sequence tag; homolog to alx3 gene product; Mesocricetus auratus" 9 others
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Winterce A.K., The Royal Veterinary and Agricultural University,
Department of Animal Science and Animal Health, Division of Animal
Genetics, Bulowsvej 13, 1870 Faceliksberg C, DENMARK
Key
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Winteroe A.K., Fredholm M., Davies W.; "Evaluation and characterization of a porcine small intestine cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            320 cagaagctcgggtacagatctggttccagantcagcgagccaagcgncggaag 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SCIEIL standard; RNA; EST; 372 BP.

SCIEIL standard; RNA; EST; 372 BP.

971739
30-40G-1995 (Rel. 45, Created)
30-50G-1996 (Rel. 49, Last updated, Version 3)
S.SCIOTA MRNA; expressed sequence tag (5'; clone clell)
EST; expressed sequence tag.
EST; expressed sequence tag.
BST; expressed sequence tag.

EST; expressed sequence tag.

EST; expressed sequence tag.

FINE SCIOTA (domestic pig)
EUR SCIOTA (Almalia; Metazoa; Chordata; Vertebrata; Mammalia; Theria; Eutherla; Artiodactyla; Suiformes; Suidae.
                                                                                                                                                                                                                                               DB 128; Length 372;
                                                                                                                                                                                                                                         Query Match 2.0%; Score 49; DB 128; Length 37: Best Local Similarity 62.4%; Pred. No. 7.98e-20; Matches 108; Conservative 0; Mismatches 65; Indels
/clone="cle11"
<1..>372
/gene="orf"
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Best Local Similarity 62.4%;
Matches 108; Conservative
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1 (bases 1 to 309)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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                                                                                                                                                                                 W81935 309 bp mRNA EST 12-SEP-1996 me93dll.rl Soares mouse embryo NbME13.5 14.5 Mus musculus CDNA clone 403125 5' similar to 9b:X52875 Mouse homeobox gene S8 mRNA
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WashD-HHMI Mouse EST Project
WashIngton University School of MedicineP
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
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Vertebrata; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae;
Gaps
                                                           320 cagaagetegggtacagatetggttecaganteagegagecaagegneggaag 372
                                                                                 /clone_lib="Soares mouse embryo NbME13.5 14.5"
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Pred. No. 3.39e-16;
0; Mismatches 59; Indels
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/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Trace considered overall poor quality
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1.309
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The WashU-HHMI Mouse EST Project
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Best Local Similarity 64.7%;
Matches 110; Conservative
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Search completed: Fri May 30 16:40:55 1997 Job time : 2071 secs.

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Thu May 29 11:34:49 1997; MasPar time 13.15 Seconds 570.251 Million cell updates/sec Run on:

abular output not generated.

Title:

Description: Perfect Score: Sequence:

.>uS-08-701-278-2 (1-263) from USO8701278.pep 1857 1 MFYFHCPPQLEGTAPFGNHS......EGSQDKPSPTKEQSEGEKSV 263

PAM 150 Gap 11 Scoring table:

89912 seqs, 28507787 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

l:annl 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3 8:unann4 9:unann5 10:unann6 11:unann7 12:unann8 13:unann9 14:unann10 15:unenc 16:unrev

Mean 44.651; Variance 107.204; scale 0.417 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	4.05e-44	5.48e-43	3.00e-40	4.35e-40	4.35e-40	4.35e-40	6.29e-40	6.29e-40	1.32e-39	2.76e-39	1.91e-39	2.76e-39	8.34e-39	8.34e-39	8.34e-39	1.74e-38	1.74e - 38	1.74e-38	2.52e-38	7.61e-38	6.90e-37
Description	transcription factor	Phox2 homeodomain pr	paired-related homeo	MHox - mouse	homeobox protein - m	DNA-binding protein	homeodomain protein	homeotic protein smo	gene alx3 protein -	transcription factor	transcription factor	pax-3 protein - mous	homeotic protein S8	gene S8 protein - mo	Prx-2 protein - chic	mab-18 protein (tran	mab-18 protein (tran	vab-3 protein - Caen	cartilage homeoprote	Pax7 - mouse (fragme	gene Pax-6 protein -
£	A46403	148713	I50413	153118	148902	S26076	151226	S27842	148185	A45452	S50115	S15031	S18038	I48410	S49440	860250	S60251	S60252	A47523	149265	151234
% Query Match Length DB	384 16	280 14	244 13	217 14	217 14	245 14	245 16	288 12	346 14	326 13	467 13	479 14	164 14	164 14	165 13	284 12	296 12	455 12	326 14	290 14	216 16
% Query Match 1	21.5	21.1	20.2	20.1	20.1	20.1	20.1	20.1	20.0	19.9	19.9	19.9	19.7	19.7	19.7	19.6	19.6	19.6	.19.5	19.4	19.1
Score	399	392	375	374	374	374	373	373	371	369	370	369	366	366	366	364	364	364	363	360	354
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Pax-6 protein - rat 6.90e-37 paired box homeotic 6.90e-37 paired box homeotic 6.90e-37 pax-6 protein - qu 6.90e-37 homeotic protein and 6.90e-37 homeotic protein and 6.90e-37 homeotic protein PAX 9.97e-37 homeotic protein PAX 9.97e-37 homeotic protein PAX 9.97e-37 homeotic protein BSH 6.23e-36 homeotic protein 6.1.30e-35 homeotic protein 6.1.30e-35 homeotic protein 6.1.30e-35 homeotic protein 6.1.30e-35 homeotic protein 7.5.60e-35 homeotic protein 7.5.60e-35 homeotic protein 7.5.60e-35 homeotic protein 7.5.60e-35 homeotic protein 90 2.41e-34 gastrulation-express 2.41e-34 homeotic protein 7.5.60e-34 homeotic protein 7.5.60e-33 reversed polarity pr 1.49e-33	ALIGNMENTS pe complete factor with prd-type homeo domain and homain-al - Drosophila brosophila sequence_revision 21-Sep-1993 #text_change spielmann, P.; Noll, M. 993) 7:114-129 etics of aristaless, a prd-type homeo box gene the morphogenesis of proximal and distal ments in a subset of appendages in Drosophila. ary acid label SCH ary acid ary acid extracted from NCBI backbone #molecular-weight 41058 #tehecksum 2627	ty 71.8%; Score 399; DB.16; Length 384; ty 71.8%; Pred. No. 4.05e-44; Servative 9; Mismatchegh.11; Indels 0; Gaps 0; tsfqleelekafsrthypdvftreelamkigiteariqvwfqnrrakwr 141 :
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#title

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GENETICS SUMMARY

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gene name Pmx
#length 217 #molecular-weight 24369
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90 KTERGA-SDQEPGA-KEPMAEVTPPPVRNINSPPP 122
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#cross-references MUID:94245205
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           D.A.; Olson, E.N.
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Best Local Similarity 54.7%;
Matches 52; Conservative
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                                   The mouse homeodomain protein Phox2 regulates Noam promoter activity in concert with Cux/CDP and is a putative determinant of neurotransmitter phenotype.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #authors Nohno, T.; Koyama, E.; Myokai, F.; Taniguchi, S.; Ohuchi,
Saito, T.; Noji, S.
#journal Dev. Biol. (1999) 158:254-264
#title The chicken homeobox gene related to Drosophila paired is
predominantly expressed in the developing limb.
#cross_references WUID:93321789
                                                                                                                                                                                                                                                                                                                                       91 krkgrrnrttfnssglgalervferthypdafvredlarrvnltearvgvwfgnrrakfr 150
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Cserjesi, P.; Lilly, B.; Bryson, L.J.; Wang, Y.; Sassoon
                                                                                                                                                                                                                                                                                                             Gaps
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02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
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#length 280 #molecular-weight 29417 #checksum 3267
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#length 244 #molecular-weight 27130 #checksum 5105
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Pred. No. 5.48e-43;
11; Mismatches 11; Indels
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##cross-references GB:D13433; NID:g222850; CDS_PID:g222851
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                                                                                                           **status preliminary; translated from GB/EMBL/DDBJ###nolecule_type mRNA
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#fresidues
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Pred. No. 3.00e-40;
16; Mismatches 25; Indels
Goridis, C.; Brunet, J.F.
Development (1993) 119:881-896
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                                                                                         cross-references MUID:9424481
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21.1%;
Best Local Similarity 69.9%;
Matches 51; Conservative
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Best Local Similarity 55.3%;
Matches 52; Conservative
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ACCESSIONS REFERENCE

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#journal Development (1992) 115:1087-1101 MHox:a mesodermally restricted homeodomain protein that binds an essential site in the muscle creatine kinase enhancer. #cross-references MUID:93083424
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A novel murine homeobox gene isolated by a tissue specific
                                                                                                                                                                                                                                                                                                                                                                        91 krkgrrnrttfnssglgalervferthypdafvredlarrvnltearvgvwfgnrrakfr 150
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homeobox protein - mouse
#formal_name Mus musculus #common_name house
02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
02-Jul-1996
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DNA-binding protein - mouse
#formal_name Mus musculus #common_name house mouse
25-Feb-1994 #sequence_revision 01-Sep-1995 #text_change
SZ6076
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Potter, S.S.
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Potter, S.S.
Genomics (1994) 19:334-340 --
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                                                                                                                                                                                                                                                                                  Length 217;
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PCR cloning strategy

*accession

95-151

SUMMARY

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gene alx3 protein - golden hamster
#formal_name Mesocricetus auratus #common_name golden hamster
02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
02-Jul-1996
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#journal Am. J. Hum. Genet. (1993) 52:455-462
#title Mutations in the paired domain of the human PAX3 gene cause Klein-Waardenburg syndrome (WS-III) as well as Waardenburg #cross-references MUID:93190976
#accession A45452
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#formal_name Homo sapiens #common_name man
21.Sep-1993 #sequence_revision 10-May-1996 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. (1994) 91:12203-12207
Pancreatic beta cells express a diverse set of homeobox
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                                                                                  #domain homeobox homology #label HOX
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#length 346 #molecular-weight 37203
                                                                                                                                                                                     17; Mismatches 22;
                                                                                                                                         Query Match 20.1%; Score 373; DB 12; Best Local Similarity 54.8%; Pred. No. 6.29e-40; Matches 51; Conservative 17; Mismatches 22
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Pred. No. 1.32e-39;
8; Mismatches 10
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FICATION #superfamily homeobox homology
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##residues 1-346 ##label RES
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    1-288 ##label WEB
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Local Similarity 71.9%;
les 46; Conservative
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#submission submitted to the EMBL Data Library, February 1992
#description, Conserved classes of homeodomains in Schistosoma mansoni, an
early bilateral metazoan.
#accessjon $27842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kuratani, S.; Martin, J.F.; Wawersik, S.; Lilly, B.; Eichele,
G.; Olson, E.N.
Dev. Biol. (1994) 161:357-369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #title The expression pattern of the chick homeobox gene gMHox suggests a role in patterning of the limbs and face and in compartmentalization of somites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         151226 #type complete
homeodomain protein - chicken
#formal_name Gallus sp. #common_name chicken
13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change
13-Sep-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mansoni) (fragment)
#formal_name_Schistosoma_mansoni
17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
30.Sep-1993
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Pred. No. 4.35e-40;
18; Mismatches 23; Indels 5
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Pred. No. 6.29e-40;
8; Mismatches 10; Indels
                                                                                                                                                              #domain homeobox homology #label HOX #length 245 #molecular-weight 27269 #ch
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                                                                                                                                                                                                                                                                                                                                                                                                                 ##residues 1-245 ##label KER ##cross-references EMBL:X59725 % CLASSIFICATION #superfamily homeobox homology FEATURE
                             ##molecule_type mRNA
                                                                                                                                                                                                                         Query Match 20.1%;
Best Local Similarity 54.7%;
Matches 52; Conservative
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Best Local Similarity 72.3%;
Matches 47; Conservative
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##molecule_type mRNA
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Opstelten, D.J.E.; Vogels, R.; Robert, B.; Kalkhoven, E.; Zwartkruis, F.; de Laaf, L.; Destree, O.H.; Deschamps, J.; Lawson, K.A.; Meijlink, F. submitted to the EMBL Data Library, May 1990
The mouse homeobox gene, S8, is expressed during embryogenesis predominantly in mesenchyme.
                                                                                                                                                                                    EMBO J. (1991) 10:1135-1147
Pax-3, a novel murine DNA binding protein expressed during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 215 lkrkqrrsrttftaegleeleraferthypdiytreelagrakltearvqvwfsnrrarw 274
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#domain homeobox homology #label HOX
#length 479 #molecular-weight 52984 #checksum 6402
                                                                                                                                                                                                                                                                                                                                 #superfamily paired box homology; homeobox homology
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Pred. No. 8.34e-39;
9; Mismatches 10; Indels
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CLASSIFICATION #superfamily homeobox homology
KEYWORDS DNA binding; homeobox
                                                                                                                                                                                                                                                                                                            1-479 ##label GOU
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nes 46; Conservative
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Nucleic Acids Res. (1994) 22:4574-4582
Molecular cloning and characterization of a human PAX-7 cDNA expressed in normal and neoplastic myocytes.
                                                          sequence modified after extraction from NCBI backbone
                                                                                                                           Genomic organization of the human PAX3 gene: DNA sequence analysis of the region disrupted in alveolar rhabdomyosarcoma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S50115 #type fragment
transcription factor pax-7 - human (fragment)
#formal_name Homo sapiens #common_name man
14-Jul-1995 #sequence_revision 10-Nov-1995 #text_change
19-Jan-1996
                                                                       A56744
Macina, R.A.; Barr, F.G.; Galili, N.; Rlethman, H.C.
Genomics (1995) 26:1-8
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Schaefer, B.W.; Czerny, T.; Bernasconi, M.; Genini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ##Fesidues 1-467 ##label SCH
##cross-references EMBL:235141
FICATION #superfamily paired box homology; homeobox homology
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##residues 1-28,29-306 ##label HOT
##cross-references NCBLN:126845; NCBIP:126846; NCBIN:126847;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 370; DB 13; Length 467; Pred. No. 1.91e-39;
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#domain homeobox homology #label HOX
#length 467 #checksum 4440
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Pred. No. 2.76e-39;
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CLASSIFICATION #superfamily homeobox homology
                                                                                                                                                                                                   ##molecule_type DNA
##residues 1-28;43-326 ##label MAC
##cross-references GB:U12263
                                         NCBIP: 126848
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Length 164;

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Brouwer, A.; Meljlink, F. submitted to the EMBL Data Library, June 1994
Expression of members of the Prx-family of homeobox genes (S8 and Mhox/K2/Pmx/Phox1) in mouse and chicken embryos.
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Prx-2 protein - chicken
#formal_name Gallus gallus #common_name chicken
20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
07-Jul-1995
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             148410 #type fragment
gene S8 protein - mouse (fragment)
#formal_name Mus musculus #common_name house mouse
02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
02-Jul-1996
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#length 165 #molecular-weight 18691 #checksum 7828
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19.7%; Score 366; DB 13; Length 165;
Best Local Similarity 70.8%; Pred. No. 8.34e-39;
Matches 46; Conservative 9; Mismatches 10; Indels
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##cross-references EMBL:X79695
FICATION #superfamily homeobox homology
                                                                                                                                                                                                                                                                                                      gene name S8
#length 164 #checksum 4472
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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

MasPar time 9.24 Seconds 603.427 Million cell updates/sec Thu May 29 11:33:55 1997; Run on:

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>US-08-701-278-2 (1-263) from USO8701278.pep 1857 1 MFYFHCPPQLEGTAPFGNHS.......EGSQDKPSPTKEQSEGEKSV 263

Description: Perfect Score: Title:

Sequence:

PAM 150 Gap 11 Scoring table:

59021 seqs, 21210388 residues Searched:

Post-processing:

Minimum Match 0% Listing first 45 summaries

Database:

swiss-prot34
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11

Mean 46.324; Variance 87.195; scale 0.531

Statistics:

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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sult.	Score	Query Match	Ouery Match Length DB	DB	a	Description	Pred. No.
-	375	20.2	244	2	HPR1 CHICK	HOMEOBOX PROTEIN PRX-	2.18e-51
~	374	20.1	199	7	PMX1 HUMAN	PAIRED MESODERM HOMEO	3.49e-51
:	374	20.1	217	7	PMX1_MOUSE	MESODERM	3.49e-51
4	370	19.9	467	7	PAX7_HUMAN		2.27e-50
S	369	19.9	479	7	PAX3_MOUSE	PAIRED BOX PROTEIN PA	3.62e-50
9	369	19.9	479	^	PAX3_HUMAN	PAIRED BOX PROTEIN PA	3.62e-50
7	360	19.4	290	7	PAX7_MOUSE	PAIRED BOX PROTEIN PA	2.42e-48
œ	357	19.2	419	.7	GSC_DROME	HOMEOBOX PROTEIN GOOS	9.79e-48
σ	354	19.1	216	7	PAX6_CHICK	PAIRED BOX PROTEIN PA	3.95e-47
10	354	19.1	416	7	PAX6_COLJA	PAIRED BOX PROTEIN PA	3.95e-47
11	354	19.1	422	7	PAX6_MOUSE	PAIRED BOX PROTEIN PA	3.95e-47
12	354	19.1	422	7	PAX6_HUMAN	PAIRED BOX PROTEIN PA	3.95e-47
13	353	19.0	437	7	PAX6_BRARE	PAIRED BOX PROTEIN PA	6.29e-47
14	353	19.0	613	2	HMPR_DROME	SEGMENTATION PROTEIN	6.29e-47
15	351	18.9	449	4	GSBP_DROME	GOOSEBERRY PROXIMAL P	1.59e-46
16	346	18.6	252	10	UNC4_CAEEL	HOMEOBOX PROTEIN UNC-	1.62e-45
17	342	18.4	245	4	GSC_CHICK	HOMEOBOX PROTEIN GOOS	1.03e-44
18	339	18.3	289	7	OTX2_MOUSE	HOMEOBOX PROTEIN OTX2	4.13e-44
19	338	18.2	256	4	GSC_MOUSE	HOMEOBOX PROTEIN GOOS	6.56e-44
20	338	18.2	289		OTX2_HUMAN	HOMEOBOX PROTEIN OTX2	6.56e-44
21	338	18.2	427	4	GSBD_DROME	GOOSEBERRY DISTAL PRO	6.56e-44
22	337	18.1	240	4	GSC_BRARE	HOMEOBOX PROTEIN GOOS	1.04e-43

- 12.10 do conceptodo

151 rnermlasknasllksysgdvtaveqpivprpap 184 : || : :: | :: | :1 | : | : | : | 90 KTERGASDQEPGA-KEPMAEVTPPPVRNINSPPP 122

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Gaps

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Query Match 20.2%; Score 375; DB 5; Length 244; Best Local Similarity 55.3%; Pred. No. 2.18e-51; Matches 52; Conservative 16; Mismatches 25; Indels

Query Match

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2.62e-43 2.62e-43 1.66e-4-43 1.66e-4-43 1.22e-32-42 1.22e-33 1.26e-33 1.26e-33 1.26e-33 1.26e-33 1.26e-36 1.74e-26 1.74e-26 1.74e-26 1.74e-26 1.74e-26 1.74e-26 1.74e-26 1.74e-26 1.74e-26 1.74e-26 1.74e-26 1.74e-26 1.74e-26
GGOOS GCOCS GCOCS GCOCS GCTX1 OCTX1 OCTX1 OCTX1 CCHO MNC - MNC - MNC - MOX - M
PROTEIN
HOMEOBOX HOM
GSCB_XENLA GSCA_XENLA GSCA_XENLA HM10_CAEEL OTX1_HOUSE HW0C_DROME HW12_CAEEL HW13_CHCAEEL HW11_MOUSE HW11_MOUSE HW11_MOUSE HW11_CAEEL HW11_DROME HW11_DROME HW11_DROME HW11_DROME HW11_DROME HW11_DROME HW11_DROME HW11_DROME HW11_DROME HW11_DROME HW11_DROME HW11_DROME HW11_DROME HW11_DROME HW11_DROME HW12_MOUSE HW12_MOUSE HW12_MOUSE HW12_MOUSE HW12_MOUSE HW12_MOUSE HW12_MOUSE HW12_MOUSE
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0 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

ALIGNMENTS

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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE;
GALLIFORMES.
                                                                                                                                                                                                                                                              DEV. BIOL. 158:254-264(1993).

-!- FUNCTION: MAY BE INVOLVED IN THE DIFFERENTIATION OF BONE, MUSCLE, and OTHER TISSUES OF MESODERMAL ORIGIN DURING LIMB DEVELOPMENT.

-!- SUBCELLULAR LOCATION: NUCLERAL DREDOMINANTLY IN THE MESODERMAL CELLS OF THE LIMB BUD, VISCERAL ARCHES AND CRANIOFACIAL PROCESS, AND AT LOWER LEVELS, IN CRANIAL MESENCHYME, UPPER AND LOWER EYELIDS, SOMITES AND CRAILIAGE OF VERTEBRA.

-!- SIMILARITY: STRONG WITH OTHER "PAIRED-TYPE" HOMEOBOX PROTEINS.
                                                                                                                                                                    [1]
SEQUENCE FROM N.A.
TISSUE-LIMB BUD;
MEDLINE; 93321789.
NOHNO T., KOYAWA E., MYOKAI F., TANIGUCHI S., OHUCHI H., SAITO T.,
                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, D13433; G222851; --
HSSP; P02836; 1ENH.
PROSITE; PS00027; HOMEOBOX:
HOMEOBOX; DNA-BINDING; DEVELOPMENTAL PROTEIN; NUCLEAR PROTEIN.
DNA_BIND 94 153 HOMEOBOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          244 AA; 27130 MW; 6BD4C3A2 CRC32;
                                       01-JUN-1994 (REL. 29, CREATED)
01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
HOMEOBOX PROTEIN PRX-1.
             244 AA
              PRT;
              STANDARD;
                                                                                                                       GALLUS GALLUS (CHICKEN)
           HPR1_CHICK
Q05437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA_BIND
SEQUENCE
RESULT
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US-08-701-278-2.rsp

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217 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE; 95075634.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 89305521.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAX7_HUMAN
P23759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                   1- FUNCTION: ACTS AS A TRANSCRIPTIONAL REGULATOR OF MUSCLE CREATINE KINASE (MCK) AND SO HAS A ROLE IN THE ESTABLISHMENT OF DIVERSE MESODERMAL MUSCLE TYPES. THE PROFEIN BINDS TO AN A/T-RICH ELEMENT IN THE MUSCLE CREATINE ENHANCER (BY SIMILARITY).
1- SUBCELLULAR LOCATION: NUCLEAR.
1- SIMILARITY: STRONG WITH OTHER "PAIRED-TYPE" HOMEOBOX PROFEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73 krkgrrnrttfnssglgalervferthypdafvredlarrvnltearvgvwfgnrrakfr 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT 3
PMYL MOUSE STANDARD: PRT; 217 AA.
P443271: 002810;
01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
PAIRED MESODERM HOMEOBOX PROTEIN I (HOMEOBOX PROTEIN MHOX) (HOMEOBOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KERN M.J., WITTE D.P., VALERIUS M.T., ARONOW B.J., POTTER S.S.;
NUCLEIC ACLIBS RES. 20:5189-5195(1992).
-1- FUNCTION: ACTS AS A TRANSCRIPTIONAL REGULATOR OF MUSCLE CREATINE
KINASE (MCK) AND SO HAS A ROLE IN THE ESTABLISHMENT OF DIVERSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30 RKKORNRTIFALGQLEALEAVFAQTHYPDVFTREELAMKINLTEARVQVWFONRRAKWR 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CSERJESI: P., LILLY B., BRYSON L., WANG Y., SASSOON D.A., OLSON E.N.; DEVELOPMENT 115:1087-1101(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE; 94245205.
KERN M.J., ARGAO E.A., BIRKENMEIER E.H., ROWE L.B., POTTER S.S.;
GENOMICS 19:334-340(1994).
                                                                                                                                                                                                    HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M95929; G189947; -.
MIM; 167420; -.
HOMEOBOX; DNA-BINDING; DEVELOPMENTAL PROTEIN; NUCLEAR PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5
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EURARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                             01-OCT-1996 (REL. 34, CREATED)
1-OCT-1996 (REL. 34, LAST ANOTATION UPDATE)
01-OCT-1996 (REL. 34, LAST ANOTATION UPDATE)
PAIRED MESODERM HOMEOBOX PROTEIN 1 (HOMEOBOX PROTEIN PHOXI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 374; DB 7; Length 199;
Pred. No. 3.49e-51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                            GRUENEBERG D.A., NATESAN S.* ALEXANDRE C., GILMAN M.Z.;
SCIENCE 257:1089-1095(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HOMEOBOX.
4E3ADE7F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : ||: :: :: | ::||: |:||
90 KTERGA-SDQEPGA-KEPMAEVTPPPVRNINSPPP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              133 rneramlanknasllksysgdvtaveqpivprpap 167
                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 1
76 135 HC
199 AA; 22455 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 20.1%;
Local Similarity 54.7%;
les 52; Conservative
                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EUTHBRIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FROM N.A.
93083424.
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 93027261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROTEIN K-2).
PMX1 OR PMX.
2
PMX1_HUMAN
P54821;
01-
                                                                           01-0CT-1996
01-0CT-1996
                                                                                                                                                               (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 93
CSERJESI P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                             MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON_TER
                 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
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IN THE MUSCLE CREATINE ENHANCER.
SUBCELLULAR LOCATION: NUCLEAR.
TISSUE SPECIFICITY: EXPRESSED EXCLUSIVELY IN MESODERMALLY DERIVED
CELL TYPES. DURING EMBRYOGENESIS, HIGHEST LEVELS OF EXPRESSION
ARE FOUND IN THE MESENCHYME AND PRECARTILAGE ELEMENTS OF THE FACE
AND HIND LIMBS. IN THE ADULT, EXPRESSION IS RESTRICTED TO SKELETAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL).
RSSSLPRCCLHEGLHNGF -> SAMATYSATCANNSPAGGI
NMANIALIALEKEKEFYSLQRNQVPTVN (IN PMX1-B).
66A77F60 CRC32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91 krkgrrnrttfnssglgalervferthypdafvredlarrvnltearvgvwfgnrrakfr 150
MESODERMAL MUSCLE TYPES. THE PROTEIN BINDS TO AN A/T-RICH ELEMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30 RKKQRRNRTTFALQQLEALEAVFAQTHYPDVFTREELAMKINLTEARVQVWFQNRRAKWR 89
                                                                                                                                                                                                                                  OUSCUE, THEART AND OIBROOM.

I DEVELOPMENTAL AND OIBROOM.

I ALTERNATIVE PRODUCTS: TWO FORMS, PMX1-A (SHOWN HERE) AND PMX1-B, ARE PRODUCED BY ALTERNATIVE SPLICING.

I STHILARITY: STRONG WITH OTHER "PAIRED-TYPE" HOMEOBOX PROTEINS. EMBL; L06502; G199584; ...

EMBL; L06502; G199584; ...

EMBL; N08975; G40125; ...

PROSITE; PSO0027; HOMEOBOX.

HOMEOBOX, DNA-BIRDING; DEVELOPMENTAL PROTEIN; NUCLEAR PROTEIN; DNA_BIRD 94 153 HOMEOBOX.

MOD_RES 197 197 PHOSPHORYLATION (BY PROTEIN KINASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1 - FUNCTION: PROBABLE TRANSCRIPTION FACTOR. IT MAY HAVE A ROLE IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- SUBCELLULAR LOCATION: NUCLEAR.
-i- SUBURIT: CAN BIND AS A HETERODIMER WITH PAX3.
-i- SIMILARIY: STRONG WITH OTHER "PAIRED-TYPE" HOMEOBOX PROTEINS.
-i- SIMILARIY: COWTAINS A PAIRED BOX DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SCHAFER B.W., CZERNY T., BERNASCONI M., GENINI M., BUSSLINGER M.; NUCLEIC ACIDS RES. 22:4574-4582(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 374; DB 7; Length 217;
Pred. No. 3.49e-51;
18; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BURRI M., TROMYOUKIS Y., BOPP D., FRIGERIO G., NOLL M.;
EMBO J. 8:1183-1190(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1991 (REL. 20, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
PAIRED BOX PROTEIN PAX-7 (HUP1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                151 rneramlanknasliksysgdvtaveqpivprpap 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     467 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24369 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 30-195 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00027; HOMEOBOX, PROSITE; PS00034; PAIRED_BOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 54.7%;
les 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Z35141; G602343; -. EMBL; X15042; E14747; -. EMBL; X15250; E14749; -. EMBL; X15251; E14751; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SAPIENS (HUMAN)
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Best Local Similarity 66.7%;
Matches 46; Conservative
                                                                                275 rk-qagang 282
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                                                                                                       89 RKTERGASD 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRACHAN T.;
                                                                                                                                                     PAX3_HUMAN
                                                                                q
                                                                                                       ğ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              213 lkrkgrrsrttftaeqleelekaferthypdiytreelagrtkltearvqvwfsnrrarw 272
                                                                                                                                                                  Gaps
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..
TRANSCRIPTION REGULATION; HOMEOBOX; DNA-BINDING; NUCLEAR PROTEIN; DEVELOPMENTAL PROTEIN; PAIRED BOX.
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE; 91216108.
GOULDING M.D., CHALEPAKIS G., DEUTSCH U., ERSELIUS J.R., GRUSS
EMBO J. 10:1135-1147(1991).
                                                                                                                                ÷
                                                                                                                                                                                                                                                                                                                                           PAX3 OR PAX-3.
MUS MUSCULUS (MOUSE).
EUKRAYOTA: METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSCRIPTION REGULATION; PAIRED BOX; DEVELOPMENTAL PROTEIN; NUCLEAR PROTEIN; DNA-BINDING; HOMEOBOX; DISEASE MUTATION.

34 159 PAIRED BOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 94010930.
VOGAN K.J., EPSTEIN D.J., TRASLER D.G., GROS P.;
GENOMICS 17:364-369(1993).
-1- FUNCTION: PROBABLE TRANSCRIPTION FACTOR ASSOCIATED WITH
                                                                                                      Score 370; DB 7; Length 467;
Pred. No. 2.27e-50;
13; Mismatches 9; Indels
                                              HOMEOBOX.
POLY-ALA.
MISSING (IN REF. 2).
1; D2C7BCBD CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 219-260 FROM N.A., AND VARIANT SPLOTCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G -> R (IN SPLOTCH).
985984B6 CRC32;
                                                                                                                                                                                                                                                          PAX3_MOUSE STANDARD; PRT; 479 AA. P24610; 01-MAR-1992 (REL. 21, CREATED) 01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE) 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE) PAIRED BOX PROTEIN PAX-3.
                                    PAIRED BOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HOMEOBOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE, 92034997.
EPSTEIN D.J., VEKEMANS M., GROS P.,
CELL 67:767-774(1991).
                                             217 276 HO
340 346 PO
151 152 MI
467 AA; 51019 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X59358; G53592; ...
EMBL; S66429; G239201; ...
EMBL; S66433; G239203; ...
PIR; S15031; S15031.
PISSP; PO2836; IENH.
PROSITE; PS000027; HOMEOBOX.
PROSITE; PS000034; PAIRED_BOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52984 MW;
                                                                                                      Query Match
Best Local Similarity 66.7%;
Watches 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                159
278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42
479 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RANSFAC; T00680; -
                                                                                                                                                                                                  273 rk-qagang 280
                                                                                                                                                                                                                        RKTERGASD 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARIANT SPLOTCH
                                  DOMAIN
DNA_BIND
DOMAIN
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA_BIND
VARIANT
SEQUENCE
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  STITIES
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19.9%; Score 369; DB 7; Length 479;

Query Match

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<u>.</u>
                                                     215 lkrkqrrsrttftaeqleeleraferthypd1ytreelaqrakltearvqvwfsnrrarw 274
                                                                             29 LRRKQRRNRTTFALQQLEALEAVFAQTHYPDVFTREELAWKINLTEARVQVWFQNRRAKW 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 95072569.
TASSABEHJI M., NEWTON V.E., LEVERTON K., TURNBULL K., SEEMANOVA E.,
KUNZE J., SPERLING K., STRACHAN T., READ A.P.;
HUM. MOL. GENET. 3:1069-1074(1994).
[10]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIJNE; 93258399.
TASSABEHJI M., READ A.P., NEWTON V.E., PATTON M., GRUSS P., HARRIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 95072569.
TASSABEHJI M., NEWTON V., LEVERTON K., TURNBULL K., SEEMANOVA E., KUNZE J., SPERLING K., STRACHAN T., READ A.; HUM. MOL. GENET. 3:1069-1074(1994).
                                                                                                                                                                                                                                                                                                                                                                                          HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARIANT WS1 LEU-50.
MEDLINE: 92168114.
BALDMIN C.T., HOTH C.F., AMOS J.A., DA-SILVA E.O., MILUNSKY
NATURE 355:637-638(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 93190976.
HOTH C.F., MILUNSKY A., LIPSKY N., SHEFFER R., CLARREN S.K.
BALDWIN C.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TASSABEHJI M., READ A.P., NEWTON V.E., HARRIS R., BALLING GRUSS P., STRACHAN T.;
NATURE 355:635-636(1992).
                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-29 AND 197-479 FROM N.A.
RIETHMAN H.C., MACINA R.A.;
SUBMITTED (JUL-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D., FRIGERIO G., NOLL
Pred. No. 3.62e-50;
13; Mismatches 9;
                                                                                                                                                                                                                                                                                            01-NOV-1991 (REL. 20, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
10-CCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
PAIRED BOX PROTEIN PAX-3 (HUP2).
                                                                                                                                                                                                                                                         479 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (PAX3A AND PAX3B).
MEDLINE: 94171226.
TSUKAMOTO K., NAKAMURA Y., NIKAWA N.;
HUM. GENET. 93:270-274(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AM. J. HUM. GENET. 52:455-462(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIANTS WS3 HIS-47 AND WS1 LEU-56.
                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /ARIANTS WS1 LEU-45 AND ASP-99.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARIANT WS1 ALA-63--ILE-67 DEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 89305521.
BURRI M., TROMVOUKIS Y., BOPP
EMBO J. 8:1183-1190(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 196-392 FROM N.A. MEDLINE; 95072569.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 30-195 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAT. GENET. 3:26-30(1993).
                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIANT WS2 ALA-81.
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ASAPQSDEGSDIDSEPDLPL -> GKRWRLGRRTCWTWRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F -> L (IN WS1).
N -> H (IN WS3).
N -> K (IN CDHS).
P -> L (IN WS1; IMPORTANT HEARING LOSS).
R -> L (IN WS1; ASSOCIATED WITH
                                                                                                                                                                                                                                                                                                                                                                                                    SAS (IN PAX3A).
MISSING (IN PAX3A).
ASAPOSDEGSD -> GKALVSGVSSH (IN PAX3B)
MISSING (IN PAX3B).
                                                                                                                                                                                                                                                              NUCLEAR PROTEIN; DISEASE MUTATION; CHROMOSOMAL TRANSLOCATION;
PROTO-ONCOGENE; ALTERNATIVE SPLICING; POLYMORPHISM.
                                                                                                                                                                       TRANSFAC; T00397; -.
TRANSFAC; T00679; -.
TRANSCRIPTION REGULATION; PAIRED BOX; DEVELOPMENTAL PROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 369; DB 7; Length 479; Pred. No. 3.62e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6EE1491D CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                V -> M (IN WS1)
M -> V (IN WS1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (IN WS1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     290 AA
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-> F (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MISSING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52967 MW;
                                                                                                                                               PAIRED_BOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 66.7%;
les 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60
67
67
88
88
85
99
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MUS MUSCULUS (MOUSE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                238
265
271
315
479 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           275 rk-qagang 282
                                                                                                                 PROSITE; PS00027;
PROSITE; PS00034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89 RKTERGASD 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 91265334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62
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                                                                                         22880
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                                                                                                                                                                                                                                                                                                                       DOMAIN
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Matches
     DORKEN CONTRACTOR CONT
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J. MED. GENET. 33:655-60(1996).

1. FUNCTION: PROBABLE TRANSCRIPTION FACTOR ASSOCIATED WITH
DEVELOPMENT OF ALVEOLAR RHADOMYOSARCOMA.

1. FUNCTION: PROBABLE TRANSCRIPTION FACTOR ASSOCIATED WITH
DEVELOPMENT OF ALVEOLAR RHADOMYOSARCOMA.

1. SUBMCELLULAR LOCATION: NUCLEAR.

1. SUBMCIT: CAN BIDD AS A HETERODITION TO THE NORMAL PAX3 PROPEIN, THE
GENE CAN PRODUCES, BY ALTERNATIVE SPLICING, TWO TRUNCATED FORMS
WHICH ARE CALLED PAX3 AND PAX3B.

2. I SUBMCELLED PAX3A AND PAX3B.

2. PROGRESSIVE SENSORY. HURDAL DEVELOR SPRINGES FRAURES
AN AUTOSOMAL DOMINANT DISORDER, CHARACTERIZED HITH NON
PROGRESSIVE SENSORY. HURDAL DEAFINESS, AS WELL AS PIGMENTARY CHANGES
OF THE IRIDES AND OF THE HAIR AND SKIN; EACH OF THE INNER CORNER OF
THE EXID. TYPE II (WS1 OR KLEIN-WAARDENBURG SYNDROME) IS
CHRARACTERIZED WITH WAS1 AND TYPE II (WS2 OR KLEIN-WAARDENBURG SYNDROME) IS
CHRARACTERIZED WITH WAS1 AND SYNDROME (CDHS), IS THOUGHT
CHAPACTERIZED WITH WAS1 AND SHARESSHEED WASILLA, SMALL AND
SHORT NOSE WITH THIN NARES, HIMPOPLASIC MAXILLA, SMALL AND
SHORT NOSE WITH THIN NARES, HIMPOPLASIC MAXILLA, SHALL AND
SHORT NOSE WITH THIN NARES, HIMPOPLASIC MAXILLA, SHALL AND
SHORT NOSE WITH THIN NARES, HIMPOPLASIC BY A
DISEASE RHABDOMYOSARCOMAL DEAFNESS.

1. DISEASE RHABDOMYOSARCOMAL DEAFNESS.

2. CHROMOSOMAL TRANSLOCATION T(2:13) (Q35,014) WHICH INVOLVES PAX3 AND
PREFERENCE OF THE WEIGHT OF THE WRIST.

2. CHROMOSOMAL TRANSLOCATION T(2:13) (Q35,014) WHICH INVOLVES PAX3 AND
PROPERED OF THE WEIGHT OF THE WEIGHT OF THE WEIGHT.

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                       MEDLINE; 95135456.
PIERPONT J.W., DOOLAN L.D., AMANN K., SNEAD G.R., ERICKSON R.P.;
HUM. MUTAT. 4:227-228(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANT LYS-315.
HOL F.A., GEURDS M.P.A., CHATKUPT S., SHUGART Y.Y., BALLING R.,
SCHRANDER-STUMPEL C.T.R.M., JOHNSON W.G., HAMEL B.C.J.,
                                                                                                                                                              MEDLINE: 95126143.
LALWANI A.K., BRISTER J.R., FEX J., GRUNDFAST K.M., PLOPLIS
SAN AGUSTIN T.B., WILCOX E.R.;
AM. J. HUM. GENET. 56:75-83(1995).
                                                                                                                                                                                                                                                                                                                                      MEDLINE; 95243235.
ZLOTOGORA J., LERER I., BAR-DAVID S., ERGAZ Z., ABELIOVICH
AM. J. HUM. GENET. 56:1173-1178(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 96263735.
ASHER J.H. JR., SOMMER A., MORELL R., FRIEDMAN T.B.;
HUM. MUTAT. 7:30-35(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANTS WS1 MET-60; GLU-85 AND SER-238.
MEDLINE; 96042708.
BALDWIN C.T., HOTH C.F., MACINA R.A., MILUNSKY A.;
AM. J. MED. GENET. 58:115-122(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- SIMILARITY: CONTAINS A PAIRED BOX DOMAIN.
EMBL; U12263; G555819; -
EMBL; U12259; G555819; -
EMBL; U12269; G555819; JOINED.
EMBL; U12260; G555819; JOINED.
EMBL; U12262; G555819; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -; NOT_ANNOTATED_CDS.
G545845; -.
G545847; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -; NOT_ANNOTATED_CDS
-; NOT_ANNOTATED_CDS
                                                                                                                                         VARIANTS WS1 PHE-265 AND GLY-271.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E224055; JOINED. E224055; JOINED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANT CDHS LYS-47.
                                                                                                                                                                                                                                                                                                                 VARIANT WS3 PHE-84.
VARIANT WS1 VAL-62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S06960;
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Indels

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-i- SUBUNIT: CAN BIND AS A HETERODIMER WITH PAX3.
-i- DEVELOPMENTAL STREES EXPRESSED SPECIFICALLY DURING THE DEVELOPMENT
OF THE WERVOUS AND MUSCULAR SYSTEM.
-i- SIMILARITY: STRONG WITH OTHER "PAIRED-TYPE" HOMEOBOX PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                         JOSTES B., WALTHER C., GRUSS.P.;
MECH. DEV. 33:27-37(1990).
-!- FUNCTION: PROBABLE TRANSCRIPTION FACTOR. IT MAY HAVE A ROLE IN
                                                                                                                                                                                                                                                  EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; RODENTIA.
01-FEB-1996 (REL. 33, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
1-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
PAIRED BOX PROTEIN PAX-7 (FRAGMENT).
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EMBL; EMBL; EMBL;

EMBL; EMBL; MBL; EMBL; S

ö

SHIFFES

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MEDLINE; 9236156.

MARTIN P., CARRIERE C., DOZIER C., QUATANNENS B., MIRABEL M.A.,
ANDENBUNDER B., STEHELIN D., SAULE S.;
ONCOGENE J.1721-1728(1992).

C. I. FUNCTION: MAY BE A TRANSCRIPTION FACTOR WITH IMPORTANT FUNCTIONS
IN EYE AND NASAL DEVELOPMENT.

C. I. SUBCELLULAR LOCATION: NUCLEAR PAIRED-TYPE" HOMEOBOX PROTEINS.
C. I. SIMILARITY: STROW WITH OTHER "PAIRED-TYPE" HOMEOBOX PROTEINS.
C. I. SIMILARITY: STROW WITH OTHER "PAIRED BOX DOMA!",
TRANSCRIPTION REGULATION; HOMEOBOX; DNA-BINDING; NUCLEAR PROTEIN;
WEND: X70475; G311772:
TRANSCRIPTION REGULATION; HOMEOBOX;
WEND: MANASCRIPTION REGULATION; PAIRED BOX.
ET DOMAIN 129 209 GGLN/GLY-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COTURNIX COTURNIX JAPONICA (JAPANESE QUAIL).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE;
GALLIFORMES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     206 lkrklgrnrtsftgegiealekeferthypdvfarerlaakidlpearigvwfsnrrakw 265
                                                               MEDILINE: 94170909.
LI H.S., YANG J.M., JACOBSON R.D., PASKO D., SUNDIN O.;
LI H.S., YANG J.M., JACOBSON R.D., PASKO D., SUNDIN O.;
LI H.S., YANG J.M., JACOBSON R.D., PASKO D., SUNDIN O.;
LI LEGILI 194(1994).
LI RIGHT AND NASAL DEVELOPMENT.
LI SUBCELLULAR LOCATION: NUCLERR.
LI SUBLICILAR LOCATION: NUCLERR.
LI SIMILARITY: STRONG WITH OTHER "PAIRED-TYPE" HOMEOBOX PROTEINS.
LI SIMILARITY: CONTAINS A PAIRED BOX DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 lkrklgrnrtsftgeglealekeferthypdvfarerlaakidlpearigvwfsnrrakw 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29 LRRKQRRNRTTFALQOLEALEAVFAQTHYPDVFTREELAMKINLTEARVQVWFQNRRAKW 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29 LRRKQRRNRTTFALQQLEALEAVFAQTHYPDVFTREELAMKINLTEARVQVWFQNRRAKW 88
                                                                                                                                                                                                                                                                                                                         EMBL, S69508; G545839; -.
TRANSCRIPTION REGULATION; HOMEOBOX; DNA-BINDING; NUCLEAR PROTEIN;
DEVELOPMENTAL PROTEIN; PAIRED BOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 354; DB 7; Length 216;
Pred. No. 3.95e-47;
18; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 354; DB 7; Length 416
Pred. No. 3.95e-47;
18; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PAIRED BOX.
GLN/GLY-RICH.
HOMEOBOX.
W; D636633C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 69 HOMEOBOX.
216 AA; 24469 MW; DAB2288B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1996 (REL. 33, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
PAIRED BOX PROTEIN PAX-6 (PAX-QNR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       416 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA_BIND 210 269 H
SEQUENCE 416 AA; 46027 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 57.1%;
Matches 44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 19.1%;
Best Local Similarity 57.1%;
Matches 44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89 RKTERGASDQEPGAKEP 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rreeklrngrrgasntp 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89 RKTERGASDQEPGAKEP 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 rreeklrngrrgasntp 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. TISSUE=NEURORETINA;
               SALLIFORMES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T 10
PAX6_COTJA
P47238;
                                                                                                                                                                                                                                                                                                                                                                                                                   NON_TER
DNA_BIND
SEQUENCE
               SO THE WAR BOUCK COURT AND SO SHEET SO SO SO SHEET SO SO SO SHEET SHEET SO SHEET SHEET SO SHEET SO SHEET 
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                                                                                                                                                                                                                                                                                                                                                                Gaps 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAX-6.
GALLUS (GALLUS (CHICKEN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE;
                                                                                                                                                                                                                                                                                                                                                                                                                   262 phl-gahhhgghhlshlghgpppkrkrrhrtifteegleqleatfdkthypdvvlregla 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 96202483.
GORIELY A., STELLA M., COFFINIER C., KESSLER D., MAILHOS C.,
GORIELY A., STELLA C.,
DESSAIN S., DESPARA C.,
DEVELOPMENT 122:1641-1650(1996).
-i- SUBCELLULAR LOCATION: NUCLEAR.
-i- SIMILARITY: STRONG WITH OTHER "PAIRED-TYPE" HOMEOBOX PROTEINS.
-1- SIMILARITY: CONTAINS A PAIRED BOX DOMAIN.
EMBL; U20792; G736381; -.
EMBL; U20792; G736381; -.
EMBL; U20792; G736381; -.
DEVELOPMENTAL PROTEIN; PAIRED BOX.
NON_TER

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<1 125 PAIRED BOX.
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                                                                                                                                                                                                                                                                                                 Score 360; DB 7; Length 290;
Pred. No. 2.42e-48;
13; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 357; DB 4; Length 419;
Pred. No. 9.79e-48;
16; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DRÓSOPHILA MELANOGASTER (FRUIT FLY).
EUKARYOTA; METAZOA; ARTHROPODA; INSECTA; DIPTERA
                                                                                                                                                                                                                                           290 AA; 32911 MW; 51176D4F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                164 169 POLY-SER.
195 199 POLY-ALA.
286 345 HOMEOBOX.
419 AA: 44949 MW; D6B80216 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PAX6_CHICK STANDARD; PRT; 216 AA. P47237. 216 AA. P47237. 216 REL. 33, CREATED) 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE) 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE) PAIRED BOX PROTEIN PAX-6 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-1996 (REL. 34, CREATE)
01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-0CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
HOMEOBOX PROTEIN GOOSECOID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          321 lkvdlkeervevwfknrrakvrkqkreeqer 351:1:1 | || || || || || || :: 68 MKINLTEARVQVWFQNRRAKWRKTERGASDQ 98
                                                                                                                                                                                          HOMEOBOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POLY-ALA
                                                                                                                                                                                                                                                                                                 Query Match 19.4%;
Best Local Similarity 65.2%;
Matches 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 49.5%;
Matches 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FBGN0022222; GSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X95420; E220356;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      237 rk-qagang 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89 RKTERGASD 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FLYBASE; FBGN
DEVELOPMENTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSC_DROME P54366;
                                                                                                                                                                                    DNA_BIND
NON_TER
SEQUENCE
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DOMAIN
DNA_BIND
SEQUENCE
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Length 416;

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01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
PAIRED BOX PROTEIN PAX-6 (OCULORHOMBIN) (ANIRIDIA, TYPE II PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAIRED BOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HOMEOBOX.
                                                                                                                                                                                                                                                                                                                                 GLASER T., WALTON D.S., MAAS R.L.;
NAT. GENET. 2:232-239(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ٠
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                                                                                                                                                                                                                                                                                                                                                                                                                           HANSON I.M., SEAWRIGHT A., HARDM.
FEKETE G., VAN HEYNINGEN V.;
HUM. MOL. GENET. 2:915-920(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00027; HOMEOBOX.
PROSITE; PS00034; PAIRED_BOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M77844; G189354; --
EMBL; M77844; G189353; --
EMBL; M93650; G189633; --
PIR; A41644; A41644.
HSSP; P02836; IENH.
                                                                              (HUMAN)
                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE; 92103673.
                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE; 94258210.
                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 93372853.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRANSFAC; T01122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISEASE MUTATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANT CYS-125
                                                                                                                                                                                                                                                                                                                                                                                           /ARIANT TRP-208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /ARIANT GLY-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CEREBELLUM
                                                                            HOMO SAPIENS
                                                            PAX6 OR AN2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               206 lkrklgrnrtsftgeglealekeferthypdvfarerlaakidlpearigywfsnrrakw 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- FUNCTION: MAY BE A TRANSCRIPTION FACTOR WITH IMPORTANT FUNCTIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IN EYE AND NASAL DEVELOPMENT.
-1- SUBCELLULAR LOCATION: NUCLEAR.
-1- DEVELOPMENTAL STAGE: EXPRESSED IN THE DEVELOPING EYE AND BRAIN.
-1- SIMILARIT: STRONG WITH OTHER "PAIRED-TYPE" HOMEOBOX PROTEINS.
-1- SIMILARIT: CONTAINS A PAIRED BOX DOWAIN.
-1- DISEASE: MUTATIONS IN PAX-6 ARE THE CAUSE OF A CONDITION KNOWN AS SMALL EYE (SEY) WHICH RESULTS IN THE COMPLETE LACK OF EYES AND NASAL PRIMORDIA.
-- EMBL; X63963; E249506; -- EMBL; X63963; E249507; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 92100191.
HILL R.E., FAVOR J., HOGAN B.L.M., TON C.C.T., SAUNDERS G.F.,
HANSON I.M., PROSSER J., JORDAN T., HASTIE N.D., VAN HEYNINGEN V.;
NATURE 354:522-525(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRANSCRIPTION REGULATION, HOMEOBOX; DNA-BINDING; NUCLEAR PROTEIN; DEVELOPMENTAL PROTEIN; PAIRED BOX; ALTERNATIVE SPLICING;
                                                                                                                                                                    PAX6 OR PAX-6 OR SEY.
MUS MUSCULUS (MOUSE).
EURARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 354; DB 7; Length 422;
Pred. No. 3.95e-47;
18; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 92120664.

WALLHER C., GENERT J.L., SIMON D., DEUTSCH U., JOSTES GOULDING M.D., PLACHOV D., BALLING R., GRUSS P.; GENOMICS 11:424-434(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRO/SER/THR-RICH.
Q -> QTHADAKVQVLDNEN.
CE46F705 CRC32;
                                                                                      01-OCT-1993 (REL. 27, CREATED)
01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
PAIRED BOX PROTEIN PAX-6.
                                                        422 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAIRED BOX.
GLN/GLY-RICH.
                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE. MEDILINE; 9249181 WALTHER C., GRUSS P.; DEVELOPMENT 113:1435-1449(1991).
                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 12
PAX6_HUMAN STANDARD;
P26367;
01-AUG-1992 (REL. 23, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00027; HOMEOBOX.
PROSITE; PS00034; PAIRED_BOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46683 MW;
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 4-131 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 19.1%;
Local Similarity 57.1%;
nes 44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             266 rreeklrngrrgasntp 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RKTERGASDQEPGAKEP 105
                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; C41061; C41061.
                                                                                                                                                                                                                                 EUTHERIA; RODENTIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                422 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P02836; 1ENH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISEASE MUTATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129
210
279
66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARIANTS IN SEY
                                    T 11
PAX6_MOUSE
P32117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RANSFAC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA_BIND
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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DOMAIN

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RESULT

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-:- SIMILARITY: STRONG WITH OTHER "PAIRED-TYPE" HOMEOBOX PROTEINS.
-:- SIMILARITY: CONTAINS A PAIRED BOX DOMAIN.
-:- DISEASE: DEPECTS: IN PAX6 ARE THE CAUGE OF ANIRIDIA, TYPE II AN AUTOSOWAL DOMINANT CONGENITAL, BILATERAL PANOCULAR DISORDER CHARACTERIZED BY COMPLETE OR PARTIAL ABSENCE OF THE FOVER AND MALPORMATIONS OF THE LENS AND ANTERIOR CHAMBER.
IT IS ALSO INVOLVED IN PETER'S ANOMALY, A CONGENITAL DEFECT OF THE ANTERIOR CHAMBER OF THE EYE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 96225435.
AZUMA N., NISHINA S., YANAGISAWA H., OKUYAMA T., YAWADA M.;
NAT. GENET. 13:141-142(1996).
-i- FUNCTION: MAX BE A TRANSCRIPTION FACTOR WITH IMPORTANT FUNCTIONS
IN EYE AND NASAL DEVELOPMENT.
                                                                                                                              TON C.C.T., HIRVONEN H., MIWA H., WELL M.M., MONAGHAN P., JORDAN T., VAN HEYNINGEN V., HASTIE N.D., MEIJERS-HEIJBOER H., DRECHEIER M., ENVER-PORCRA B., COLLINS F., SWAROOP A., STRONG L.C., SAUNDERS G.F.; CELL 67:1059-1074(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (IN PETER'S ANOMALY).
(IN ISOLATED FOVEAL HYPOPLASIA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- SUBCELLULAR LOCATION: NUCLEAR.
-i- DEVELOPMENTAL STAGE: EXPRESSED IN THE DEVELOPING EYE AND BRAIN.
-i- TISSUE SPECIFICITY: FETAL EYE, OLFACTORY BULBS, RND IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSCRIPTION REGULATION; HOMEOBOX; DNA-BINDING; NUCLEAR PROTEIN; DEVELOPMENTAL PROTEIN; PAIRED BOX; ALTERNATIVE SPLICING;
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HARDMAN K., HODGSON S., ZALETAYEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 94214497.
HANSON I.M., FLETCHER J.M., JORDAN T., BROWN A., TAYLOR D.,
ADAMS R.J., PUNNET H.H., VAN HEYNINGEN V.;
NAT. GENET. 6:168-173(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (IN ANIRIDIA).
(IN REF. 2).
4AA8 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLN/GLY-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              634E4AA8
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317
422 AA;
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CONFLICT
SEQUENCE
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89 RKTER 93

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Length 422;

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SEQUENCE FROM N.A.
MEDLINE; 87051745.
FRIGERIO G., BURRI M., BOPP D., BAUMGARTNER S., NOLL M.;
CELL 47:735-746(1986).
-!- FUNCTION: PRD IS A PAIR-RULE PROTEIN REQUIRED FOR SEGMENTATION IN DROSOPHILA. CAPABLE OF SEQUENCE-SPECIFIC DNA-BINDING.
-!- SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     202 esepgialkrkgrrcrttfsasgldelerafertgypdlytreelagrtnltearigvwf 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23 DFDDGF-LRRKQRRNRTTFALQQLEALEAVFAQTHYPDVFTREELAMKINLTEARVQVWF 81
                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: STRONG WITH OTHER "PAIRED-TYPE" HOMEOBOX PROTEINS.
-!- SIMILARITY: CONTRINS A PAIRED BOX DOMAIN.
EMBL; M14548; G158160;
-PIR; A26062; A26062.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 12-145 AND 162-241 FROM N.A.
MEDLINE; 87051758.

MEDLINE; BORRI M.;
CELL 47:1033-1040(1986).

-i - FUNCTION: GOOSEBERRY DISTAL AND PROXIMAL ARE SEGMENT -POLARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANGEAC; TO0699; --
TRANGEAC; TO0699; --
HOMEDBOX; DNA-BINDING; DEVELOPHENTAL PROTEIN; NUCLEAR PROTEIN;
HOMEDBOX; REPEAT; PAIR-RULE PROTEIN; TRANSCRIPTION REGULATION.

21 PAIRED BOX.
DNA_IN 21 272 HOMEOBOX.
DNA_IN 552 572 10 X 2 AA TANDEM REPEATS OF H-P.
VARIANT 164 A -> I.
VARIANT 220 220 F -> I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
19.0%; Score 353; DB 5; Length 613;
Best Local Similarity 47.1%; Pred. No. 6.29e-47;
Matches 49; Conservative 26; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        262 snrrarlrkqhtsvsggapggaaasvshvaassslpsvvssvps 305
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DROSOPHILA MELANOGASTER (FRUIT FLY).
EUKARYOTA; METAZOA; ARTHROPODA; INSECTA; DIPTERA.
                                                                                                                                                                         DROSOPHILA MELANOGASTER (FRUIT FLY).
EUKARYOTA; METAZOA; ARTHROPODA; INSECTA; DIPTERA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0922346E CRC32;
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01-NOV-1988 (REL. 09, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
                                                                                    01-JAN-1988 (REL. 06, CREATED)
01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BAUMGARTNER S., BOPP D., BURRI M., NOLL M.;
GENES DEV. 1:1247-1267(1987).
                                                      613 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GOOSEBERRY PROXIMAL PROTEIN (BSH4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65497 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP, P02836; IENH.
FLYBASE; FBGN0003145; PRD.
PROSITE; PS00027; HOMEOBOX.
PROSITE; PS00034; PAIRED_BOX.
                                                                                                                          01-FEB-1995 (REL. 31, LAST AL
SEGMENTATION PROTEIN PAIRED.
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                                                      STANDARD;
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164
120
220
613 AA;
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GSBP_DROME
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HMPR_DROME
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SEQUENCE
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                                     Gaps
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EMBO J. 10:3609-3619(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- TISSUE SPECIFICITY: SPATIALLY RESTRICTED REGIONS OF THE NEURAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- SIMILARITY: STRONG WITH OTHER "PAIRED-TYPE" HOMEOBOX PROTEINS.
1- SIMILARITY: CONTAINS A PAIRED BOX DOMAIN.
EMBL; X61389; G62549; --
EMBL; X63183; G62547; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BRACHYDANIO RERIO (ZEBRAFISH) (ZEBRA DANIO).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PISCES; GNATHOSTOMATA;
OSTEICHTHYES; ACTINOPTERYGII; CYPRINIFORMES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 353; DB 7; Length 437; Pred. No. 6.29e-47; 12; Mismatches 10; Indels
Score 354; DB 7; Length 422
Pred. No. 3.95e-47;
18; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SER/THR/PRO-RICH.
Q -> QTHADAKVQVLDNEN.
6 6A50EC83 CRC32;
                                                                                                                                                                                                                                      PAX6_BRARE STANDARD; PRT; 437 AA. P26630; 01-802-1992 (REL. 23, CREATED) 01-802-1992 (REL. 23, LAST SEQUENCE UPDATE) 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE) PAIRED BOX PROTEIN PAX[ZF-A] (PAX-6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 91375540.
KRAUSS S., JOHANSON T., KORZH V., FJOSE A.;
NATURE 353:267-270(1991).
                                                                                                                                                                                                                                                                                                                                                  PAX[ZE-A].
BRACHYDANIO RERIO (ZEBRAFISH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   298 437
66 66
437 AA; 48425 MW;
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Local Similarity 66.2%;
hes 43; Conservative
 Query Match
Best Local Similarity 57.1%;
Matches 44; Conservative
                                                                                                                                        266 rreeklrngrrgasntp 282
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KRAUSS S., JOHANS
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